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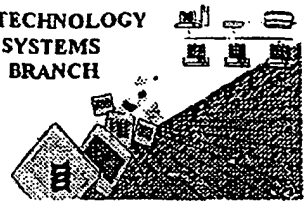

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/660,499
Source: IFW0
Date Processed by STIC: 2/24/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS..
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/1.3/03: **TELEPHONE: 571-272-2510; FAX: 571-273-0221**

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http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission User Manual** - ePAVE)
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Revised 10/08/03

IFWO

RAW SEQUENCE LISTING DATE: 02/24/2004
PATENT APPLICATION: US/10/660,499 TIME: 09:43:29

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

3 <110> APPLICANT: Seoul National University Industry Foundation
5 <120> TITLE OF INVENTION: ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
6 AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
8 <130> FILE REFERENCE: 20020-02USA
10 <140> CURRENT APPLICATION NUMBER: US 10/660,499
11 <141> CURRENT FILING DATE: 2003-09-12
13 <150> PRIOR APPLICATION NUMBER: KR 2003-19069
14 <151> PRIOR FILING DATE: 2003-03-27
16 <160> NUMBER OF SEQ ID NOS: 9
18 <170> SOFTWARE: KopatentIn 1.71

pp 1-4

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

225 <210> SEQ ID NO: 9
226 <211> LENGTH: 29
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Primer
234 <400> SEQUENCE: 9
235 agcaagcttg gagttgatgg gaataatca 29
E--> 239 (1) delete

see pp 2-3 for more errors

<400> 1
gcacgagctt caacctctca tcattaggca ttcagcaagc aagaaaaaaa a 51

atg ggc aaa atc atg ctt gtt ttg ggt agc ctc att gga tta tgc tgt 99
Met Gly Lys Ile Met Leu Val Leu Gly Ser Leu Ile Gly Leu Cys Cys
1 5 10 15
ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc 147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
20 25 30

sample of invalid amino acid placement in Sequence 1.

Per 1.822 of Sequence Rules, insert only one space between codons and amino acids; also, place amino acid directly under its codon

<210> 3
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

see p. 4 for error explanation

<400> 3
nnggatccga ygcntcnggn acnatgggyg gygctgygyt angg 44

<210> 4
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

see p.4

<400> 4
nnggatcctt kswytgccar ttnnnsncccc arttnck 37

<210> 5
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

see p.4

<400> 5
gaygcnwsng gnacnatggg nggngcntgy ggntayggna ayytntaygc nacnggntay 60
ggnacnmgna cnggcnggnyt nwsnacnggn ytnttyaayg ayggngcnws ntgyggncar 120
tgytayaara thathtgyga ytayaarwsn gaywsnmgnt ggtgyathaa rggnmgnwsn 180
gtnacnggtn cnggcnacnaa yttytgycnn cnaayttyg cnytncnaa yaayaayggn 240
ggntggtgya aycnncnnyt naarcaytty gayatggcnc arcngcntg ggaraarath 300
ggnathtaym cnggnggnat hgtncnngtn ytnttycarm gngtncntg yaaraarcay 360
ggnggnntnm gnttywsngt naayggnmgn gaytayttyg arytngtnyt nathwsnaay 420
gtnggnggng cnggnwsnat hcarwsngtn ttyathaarg gnwsnaarac nggntggatg 480
gcnatgwsnm gnaaytgggg nwsnaaytgg carwsnaay 519

4

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/660,499

DATE: 02/24/2004
TIME: 09:43:30

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

error explanation

Use of n's or Xaa's (NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:3; N Pos. 1,2,14,17,20,23,42
Seq#:4; N Pos. 1,2,23,24,26,35
Seq#:5; N Pos. 6,9,12,15,21,24,27,33,39,45,51,54,57,63,66,69,72,75,78,81,84
Seq#:5; N Pos. 87,90,93,105,108,111,117,150,156,159,174,177,180,183,186,189
Seq#:5; N Pos. 192,195,198,210,213,222,225,228,240,243,255,258,261,279,285
Seq#:5; N Pos. 288,303,312,315,318,324,327,330,333,342,345,348,363,366,369
Seq#:5; N Pos. 372,378,381,387,390,405,408,411,417,423,426,429,432,435,438
Seq#:5; N Pos. 447,450,462,465,471,474,483,489,492,501,504,516

VERIFICATION SUMMARY DATE: 02/24/2004
PATENT APPLICATION: US/10/660,499 TIME: 09:43:30

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02242004\J660499.raw

L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:3
L:139 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:3
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:152 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:4
L:152 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:4
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:165 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:165 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:239 M:254 E: No. of Bases conflict, this line has no nucleotides.